

GenCore version 5.1.4_p5_4578
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score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

OM nucleic - nucleic search, using sw model
 Run on: March 26, 2003, 11:15:29 ; Search time 9316.36 Seconds
 (without alignments)
 (without alignments)
 65.601 Million cell updates/sec
Title: US-10-086-184-2
Perfect score: 21
Sequence: gtgtctactgatagagtgtacc 21
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 205640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 774614
Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database :

- 1: GenBmbl:*
- 2: gb_ba:*
- 3: gb_hrg:*
- 4: gb_in:*
- 5: gb_om:*
- 6: gb_oov:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_stb:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vl:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ovr:*
- 23: em_patt:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sib:*
- 28: em_vl:*
- 29: em_vn:*
- 30: em_hrg_hum:*
- 31: em_hrg_inv:*
- 32: em_hrg_other:*
- 33: em_hrg_mus:*
- 34: em_hrg_pln:*
- 35: em_hrg_rod:*
- 36: em_hrg_main:*
- 37: em_hrg_vrt:*
- 38: em_sv:*
- 39: em_hrgo_hum:*
- 40: em_hrgo_mus:*
- 41: em_hrgo_other:*

Result No.	Score	Query Match	Length	DB ID	Description
C 1	13.6	64.8	25	6 AX328796	AX328796 Sequence
C 2	13.4	63.8	21	6 AX019207	AX019207 Sequence
C 3	12.8	61.0	39	6 AX418584	AX418584 Sequence
C 4	12.6	60.0	27	6 AR084832	AR084832 Sequence
C 5	12.4	59.0	17	6 A20005	A20005 SEQ ID NO:
C 6	12.4	59.0	17	6 A20013	A20013 SEQ ID NO:
C 7	12.4	59.0	17	6 A20029	A20029 SEQ ID NO:
C 8	12.4	59.0	17	6 I13201	I13201 Sequence 23
C 9	12.4	59.0	17	6 I13217	I13217 Sequence 45
C 10	12.4	59.0	20	6 AX417158	AX417158 Sequence
C 11	12.4	59.0	23	6 AX417148	AX417148 Sequence
C 12	12.4	59.0	31	6 AX417152	AX41715 Sequence
C 13	12.4	59.0	32	6 AR175460	AR175460 Sequence
C 14	12.4	59.0	34	6 AX417156	AX417156 Sequence
C 15	12.2	58.1	24	6 AX413895	AX413895 Sequence
C 16	12.2	58.1	25	6 AX447871	AX447871 Sequence
C 17	12.2	58.1	26	6 AX038056	AX038056 Sequence
C 18	12.2	58.1	26	6 AX038057	AX038057 Sequence
C 19	12.2	58.1	26	6 AX327886	AX327886 Sequence
C 20	12.2	58.1	27	6 E36449	E36449 DNA polymer
C 21	12.2	58.1	27	6 I13350	I13350 Sequence 7
C 22	12.2	58.1	32	6 I18872	I18872 Sequence 18
C 23	12.2	58.1	32	6 I36798	I36798 Sequence 18
C 24	12.2	58.1	32	6 I56002	I56002 Sequence 18
C 25	12.2	58.1	33	6 E36466	E36466 DNA polymer
C 26	12.2	58.1	35	6 AX120003	AX120003 Sequence
C 27	12.2	58.1	40	6 AX107556	AX107556 Sequence
C 28	12	57.1	22	6 A22025	A22025 Oligonucleo
C 29	12	57.1	32	6 AR093406	AR093406 Sequence
C 30	12	57.1	24	6 AR172153	AR172153 Sequence
C 31	12	57.1	24	6 BD000281	BD000281 Oligonucle
C 32	12	57.1	24	6 BD000359	BD000359 Method fo
C 33	12	57.1	24	6 BD000795	BD000795 Oligonucle
C 34	12	57.1	24	6 E30931	E30931 Amplificati
C 35	12	57.1	25	6 AX190307	AX190307 Sequence
C 36	12	57.1	33	6 I86650	I86650 Sequence 29
C 37	12	57.1	37	6 AR18187	AR18187 Sequence
C 38	11.8	56.2	20	6 AR016119	AR016119 Sequence
C 39	11.8	56.2	20	6 AR019117	AR019117 Sequence
C 40	11.8	56.2	20	6 AX293144	AX293144 Sequence
C 41	11.8	56.2	20	6 EO7026	EO7026 Primer. 9/1
C 42	11.8	56.2	22	6 AR108179	AR108179 Sequence
C 43	11.8	56.2	22	6 AR148629	AR148629 Sequence
C 44	11.8	56.2	22	6 AR206680	AR206680 Sequence
C 45	11.8	56.2	22	6 AX085790	AX085790 Sequence

ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
1	AX328796	Sequence 293 from Patent EP1164203.	AX28796	25 bp	DNA	linear	PAT 08-JAN-2002

FEATURES	SEQUENOM, INC. (US)
Source	Location/Qualifiers 1. .25 /organism="unidentified" /db_xref="Taxon:32644"
BASE COUNT	8 a 6 c 4 g 7 t
ORIGIN	
Query Match	64.8%; Score 13.6; DB 6; Length 25;
Best Local Similarity	80.0%; Pred. No. 1.7e+04; Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY	1 GRGCTACTGTAGATGGTAC 20
Db	20 GTCCTACTGTAGATAATTAC 1
RESULT 2	
AX019207/c	
LOCUS	AX019207 21 bp DNA
DEFINITION	Sequence 45 from Patent WO9941393.
ACCESSION	AX019207
VERSION	AX019207.1 GI:1.00e1239
KEYWORDS	synthetic construct. artificial sequences.
ORGANISM	' synthetic construct. synthetic construct. artificial sequences.
SOURCE	
REFERENCE	1 (bases 1 to 21)
AUTHORS	Acland,D.P.; Blake,A.N.; Lee,M.D.; Osborn,R.W.; Robinson,M.P. and Windass,J.D.
TITLE	Insecticidal peptides
JOURNAL	Patent: WO 9941393-A 45 19-AUG-1999; ACLAND DAVID PAUL (GB); BLAKE ANDREW NICHOLAS (GB); LEE MICHAEL DAVID (GB); OSBORN RUPERT WILLIAM (GB); ZENECA LTD (GB); ROBINSON MICHAEL PETER (GB); WINDASS JOHN DAVID (GB)
FEATURES	
Source	/organism="synthetic construct" /db_xref="taxon:32630" /note="primer"
BASE COUNT	5 a 5 c 5 g 6 t
ORIGIN	
Query Match	63.8%; Score 13.4; DB 6; Length 21;
Best Local Similarity	93.3%; Pred. No. 2.2e+04; Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 GCGCTACTGTAGAG 15
Db	18 GGCTTACTGTAGATGAG 4
RESULT 3	
AX418584	
LOCUS	AX418584 39 bp DNA
DEFINITION	Sequence 70 from Patent WO200006.
ACCESSION	AX418584
VERSION	AX418584.1 GI:21523449
KEYWORDS	synthetic construct. artificial sequences.
SOURCE	
ORGANISM	' synthetic construct. synthetic construct. artificial sequences.
FEATURES	
REFERENCE	1 Lu,Y. and Lin,J.
AUTHORS	Nucleic acid enzyme biosensor for ions
TITLE	Patent: WO 0200005-A 70 03-JAN-2002; THE BOARD OF TRUSTEES OF THE UNIVERSITY OF ILLINOIS (US)
JOURNAL	Location/Qualifiers
FEATURES	
Source	1. .39 /organism="synthetic construct" /db_xref="taxon:32630" /note="Zn-DNA"
BASE COUNT	10 a 5 c 9 g 15 t
RESULT 4	
AR084832/c	
LOCUS	AR084832 27 bp DNA
DEFINITION	Sequence 16 from Patent US 5981225.
ACCESSION	AR084832
VERSION	AR084832.1 GI:1.00e1603
KEYWORDS	
ORGANISM	Unknown.
SOURCE	Unclassified.
REFERENCE	1 (bases 1 to 27)
AUTHORS	Kochanek,S. and Schiedner,G.
TITLE	Gene transfer vector, recombinant adenovirus particles containing the same, method for producing the same and method of use of the same
JOURNAL	Patent: US 5981225-A 16 09-Nov-1999;
FEATURES	
Source	/organism="unknown"
BASE COUNT	11 a 5 c 5 g 6 t
ORIGIN	
Query Match	60.0%; Score 12.6; DB 6; Length 27;
Best Local Similarity	78.9%; Pred. No. 6.1e+04; Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY	1 GCGCTACTGTAGAGTGA 19
Db	24 GGTTTACTCATAGCGCTA 6
RESULT 5	
A20005/c	
LOCUS	A20005 17 bp DNA
DEFINITION	SEQ ID NO: 13; Oligonucleotide BB3510.
ACCESSION	A20005
VERSION	A20005.1 GI:1.247838
KEYWORDS	
SOURCE	
ORGANISM	' synthetic construct. synthetic construct. artificial sequences.
FEATURES	
Source	1. .17 /organism="synthetic construct" /db_xref="taxon:32630"
BASE COUNT	7 a 4 c 2 g 4 t
ORIGIN	
Query Match	59.0%; Score 12.4; DB 6; Length 17;
Best Local Similarity	92.9%; Pred. No. 8.1e+04; Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	2 TGCCTACTGTAGAG 15
Db	14 TGCTTACTGTAGTG 1
RESULT 6	
A20013/c	
LOCUS	A20013 17 bp DNA
DEFINITION	SEQ ID NO: 21; Oligonucleotide BR3510.
ACCESSION	A20013
BASE COUNT	10 a 5 c 9 g 15 t
RESULT 7	
A20014/c	
LOCUS	A20014 17 bp DNA
DEFINITION	SEQ ID NO: 22; Oligonucleotide BR3510.
ACCESSION	A20014
BASE COUNT	10 a 5 c 9 g 15 t

VERSION	A20013.1	GI	1124846
KEYWORDS	synthetic construct.		
SOURCE	synthetic construct.		
ORGANISM	artificial sequences.		
FEATURES	Location/Qualifiers		
SOURCE	1. . 17 /organism="synthetic construct" /db_xref="taxon:32630"		
BASE COUNT	7 a 4 c 2 g 4 t		
ORIGIN	Best Local Similarity 92.9%; Pred. No. 8.1e+04; 0; Mismatches 1; Indels 0; Gaps 0;		
Qy	2 TGCTACTGTAGAG 15		
Db	14 TGCTACTGTAGTG 1		
RESULT 7			
A20029/c			
LOCUS	A20029		
DEFINITION	SEQ ID NO: 37: Oligonucleotide primer BB3510.		
ACCESSION	A20029		
VERSION	A20029.1 GI:1247864		
KEYWORDS	synthetic construct.		
SOURCE	synthetic construct.		
ORGANISM	artificial sequences.		
FEATURES	Location/Qualifiers		
SOURCE	1. . 17 /organism="synthetic construct" /db_xref="taxon:32630"		
BASE COUNT	7 a 4 c 2 g 4 t		
ORIGIN	Query Match Similarity 92.9%; Pred. No. 8.1e+04; 0; Mismatches 1; Indels 0; Gaps 0;		
Qy	2 TGCTACTGTAGAG 15		
Db	14 TGCTACTGTAGTG 1		
RESULT 7			
A20029/c			
LOCUS	A20029		
DEFINITION	SEQ ID NO: 37: Oligonucleotide primer BB3510.		
ACCESSION	A20029		
VERSION	A20029.1 GI:1247864		
KEYWORDS	synthetic construct.		
SOURCE	synthetic construct.		
ORGANISM	artificial sequences.		
FEATURES	Location/Qualifiers		
SOURCE	1. . 17 /organism="synthetic construct" /db_xref="taxon:32630"		
BASE COUNT	7 a 4 c 2 g 4 t		
ORIGIN	Query Match Similarity 92.9%; Pred. No. 8.1e+04; 0; Mismatches 1; Indels 0; Gaps 0;		
Qy	2 TGCTACTGTAGAG 15		
Db	14 TGCTACTGTAGTG 1		
RESULT 7			
A20029/c			
LOCUS	A20029		
DEFINITION	SEQ ID NO: 37: Oligonucleotide primer BB3510.		
ACCESSION	A20029		
VERSION	A20029.1 GI:1247864		
KEYWORDS	synthetic construct.		
SOURCE	synthetic construct.		
ORGANISM	artificial sequences.		
FEATURES	Location/Qualifiers		
SOURCE	1. . 17 /organism="synthetic construct" /db_xref="taxon:32630"		
BASE COUNT	7 a 4 c 2 g 4 t		
ORIGIN	Query Match Similarity 92.9%; Pred. No. 8.1e+04; 0; Mismatches 1; Indels 0; Gaps 0;		
Qy	2 TGCTACTGTAGAG 15		
Db	14 TGCTACTGTAGTG 1		
RESULT 8			
I13201/c			
LOCUS	I13201		
DEFINITION	Sequence 23 from patent US 5434073.		
ACCESSION	I13201		
VERSION	I13201.1 GI:910549		
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 17)		
AUTHORS	Dawson,K., Hunter,M.G. and Czaplewski,L.G.		
TITLE	Fibrinolytic and anti-thrombotic cleavable dimers		
JOURNAL	Patent: US 5434073-A 23-18-JUL-1995; Location/Qualifiers		
FEATURES	1. . 17 /organism="unknown"		
SOURCE	/organism="unknown"		
BASE COUNT	7 a 4 c 2 g 4 t		
ORIGIN	Query Match Similarity 92.9%; Pred. No. 8.1e+04; 0; Mismatches 1; Indels 0; Gaps 0;		
Qy	6 ACTATAGACTGTA 19		
Db	20 AGTGTAGAGTGTA 7		
RESULT 11			
AX417148			
LOCUS	AX417148		
DEFINITION	Sequence 25 from Patent WO0220811.		
ACCESSION	AX417148		
VERSION	AX417148.1 GI:21449735		
KEYWORDS			
SOURCE	synthetic construct.		
ORGANISM	synthetic construct.		
RESULT 11			
AX417148			
LOCUS	AX417148		
DEFINITION	Sequence 25 from Patent WO0220811.		
ACCESSION	AX417148		
VERSION	AX417148.1 GI:21449735		
KEYWORDS			
SOURCE	synthetic construct.		
ORGANISM	synthetic construct.		

REFERENCE artificial sequences.

1 AUTHORS Golovko,A. and Hall,G.J.

TITLE Modified tet -inducible system for regulation of gene expression in

plants

PATENT: WO 0220811-A 25 14-MAR-2002;

JOURNAL BASF Plant Science GmbH (DE)

FEATURES Location/Qualifiers

1..23

/organism="synthetic construct"

/db_xref="taxon:32630"

BASE COUNT 7 a

ORIGIN 5 c

5 g

6 t

REFERENCE BASE COUNT 12 a 2 c 9 g 9 t

ORIGIN AX417156

Query Match 59.0%; Score 12.4; DB 6; Length 32;

DEFINITION Best Local Similarity 92.9%; Pred. No. 7.9e+04; Length 32;

ACCESSION Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

VERSION AX417156.1 GI:21449743

KEYWORDS synthetic construct.

SOURCE synthetic construct.

ORGANISM artificial sequences.

1

AUTHORS Golovko,A. and Hall,G.J.

TITLE Modified tet -inducible system for regulation of gene expression in

plants

PATENT: WO 0220811-A 33 14-MAR-2002;

JOURNAL BASF Plant Science GmbH (DE)

FEATURES Location/Qualifiers

1..36

SOURCE /organism="synthetic construct"

BASE COUNT 10 a

ORIGIN 7 c

5 g

14 t

REFERENCE BASE COUNT 12 a 2 c 9 g 9 t

ORIGIN AX443895/c

Query Match 59.0%; Score 12.4; DB 6; Length 36;

DEFINITION Best Local Similarity 92.9%; Pred. No. 7.8e+04; Length 36;

ACCESSION Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

VERSION AX443895.1 GI:21691173

KEYWORDS synthetic construct.

SOURCE synthetic construct.

ORGANISM artificial sequences.

1

AUTHORS Gunderson,K.

TITLE Probes and decoder oligonucleotides

JOURNAL Patent: WO 0216649-A 350 28-FEB-2002;

ILLUMINA, Inc. (US)

FEATURES Location/Qualifiers

1..24

SOURCE /organism="synthetic construct"

/db_xref="taxon:32630"

/note="Computer Generated Probe Sequence."

BASE COUNT 4 a

ORIGIN 9 c

5 g

6 t

REFERENCE BASE COUNT 12 a 2 c 9 g 9 t

ORIGIN Query Match 58.1%; Score 12.2; DB 6; Length 24;

DEFINITION Best Local Similarity 82.4%; Pred. No. 1e+05; Length 24;

ACCESSION Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

VERSION AR175460.1 GI:17916759

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

1 (bases 1 to 32)

AUTHORS Livak,K.J., Lowe,A.L. and Blashard,A.J.

TITLE Length determination of nucleic acid repeat sequences by

JOURNAL Patent: US 6309829-A 23 30-OCT-2001;

FEATURES Location/Qualifiers

1..32

SOURCE /organism="unknown"

/db_xref="taxon:32630"

BASE COUNT 4 a

ORIGIN 9 c

5 g

6 t

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Db 18 GCAACTGGTAGAGCCTA 2

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Job time : 9318.36 SECs

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